

PTO/PCT Rec'd 23 JUL 2001

SEQUENCE LISTING

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<120> Method for screening compounds inhibiting signal
transduction through inflammatory cytokines

<130> 06501-076001

<140> 09/830,144

<141> 2001-04-20

<150> PCT/JP99/05817

<151> 1999-10-21

<150> JP 10/299962

<151> 1998-10-21

<160> 10

<170> PatentIn version 2.0

<210> 1

<211> 2656

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (183)..(1919)

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gggtctcacc cggattgtcc ggggtggcacc gttcccggcc ccaccgggcg ccgcgaggga 180

tc atg tct aca gcc tct gcc gcc tcc tcc tcc tcc tcc tcc tcc gcc 227

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Gly Glu Met Ile Glu Ala Pro Ser Gln Val Leu Asn Phe Glu Glu Ile

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gac tac aag gag atc gag gtg gaa gag gtt gtt gga aga gga gcc ttt 323

Asp Tyr Lys Glu Ile Glu Val Glu Glu Val Val Gly Arg Gly Ala Phe

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Gly Val Val Cys Lys Ala Lys Trp Arg Ala Lys Asp Val Ala Ile Lys

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55

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Gln Ile Glu Ser Glu Ser Glu Arg Lys Ala Phe Ile Val Glu Leu Arg	
65 70 75	
cag tta tcc cgt gtg aac cat cct aat att gta aag ctt tat gga gcc	467
Gln Leu Ser Arg Val Asn His Pro Asn Ile Val Lys Leu Tyr Gly Ala	
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Leu Tyr Asn Val Leu His Gly Ala Glu Pro Leu Pro Tyr Tyr Thr Ala	
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Ala His Ala Met Ser Trp Cys Leu Gln Cys Ser Gln Gly Val Ala Tyr	
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Leu His Ser Met Gln Pro Lys Ala Leu Ile His Arg Asp Leu Lys Pro	
145 150 155	
cca aac tta ctg ctg gtt gca ggg ggg aca gtt cta aaa att tgt gat	707
Pro Asn Leu Leu Leu Val Ala Gly Gly Thr Val Leu Lys Ile Cys Asp	
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Phe Gly Thr Ala Cys Asp Ile Gln Thr His Met Thr Asn Asn Lys Gly	
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Ser Ala Ala Trp Met Ala Pro Glu Val Phe Glu Gly Ser Asn Tyr Ser	
195 200 205	
gaa aaa tgt gac gtc ttc agc tgg ggt att att ctt tgg gaa gtg ata	851
Glu Lys Cys Asp Val Phe Ser Trp Gly Ile Ile Leu Trp Glu Val Ile	
210 215 220	
acg cgt cgg aaa ccc ttt gat gag att ggt ggc cca gct ttc cga atc	899
Thr Arg Arg Lys Pro Phe Asp Glu Ile Gly Gly Pro Ala Phe Arg Ile	
225 230 235	
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Met Trp Ala Val His Asn Gly Thr Arg Pro Pro Leu Ile Lys Asn Leu	
240 245 250 255	
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Pro Lys Pro Ile Glu Ser Leu Met Thr Arg Cys Trp Ser Lys Asp Pro	
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Ser Gln Arg Pro Ser Met Glu Glu Ile Val Lys Ile Met Thr His Leu	
275 280 285	

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Met Arg Tyr Phe Pro Gly Ala Asp Glu Pro Leu Gln Tyr Pro Cys Gln	
290 295 300	
tat tca gat gaa gga cag agc aac tct gcc acc agt aca ggc tca ttc	1139
Tyr Ser Asp Glu Gly Gln Ser Asn Ser Ala Thr Ser Thr Gly Ser Phe	
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Met Asp Ile Ala Ser Thr Asn Thr Ser Asn Lys Ser Asp Thr Asn Met	
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Leu Leu Lys Asn Gln Ala Lys Gln Gln Ser Glu Ser Gly Arg Leu Ser	
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Leu Gly Ala Ser His Gly Ser Ser Val Glu Ser Leu Pro Pro Thr Ser	
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Glu Gly Lys Arg Met Ser Ala Asp Met Ser Glu Ile Glu Ala Arg Ile	
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gcc gca acc aca ggc aac gga cag cca aga cgt aga tcc atc caa gac	1427
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Leu Thr Val Thr Gly Thr Glu Pro Gly Gln Val Ser Ser Arg Ser Ser	
420 425 430	
agt ccc agt gtc aga atg att act acc tca gga cca acc tca gaa aag	1523
Ser Pro Ser Val Arg Met Ile Thr Thr Ser Gly Pro Thr Thr Glu Lys	
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cca act cga agt cat cca tgg acc cct gat gat tcc aca gat acc aat	1571
Pro Thr Arg Ser His Pro Trp Thr Pro Asp Asp Ser Thr Asp Thr Asn	
450 455 460	
gga tca gat aac tcc atc cca atg gct tat ctt aca ctg gat cac caa	1619
Gly Ser Asp Asn Ser Ile Pro Met Ala Tyr Leu Thr Leu Asp His Gln	
465 470 475	
cta cag cct cta gca ccg tgc cca aac tcc aaa gaa tct atg gca gtg	1667
Leu Gln Pro Leu Ala Pro Cys Pro Asn Ser Lys Glu Ser Met Ala Val	
480 485 490 495	
ttt gaa cag cat tgt aaa atg gca caa gaa tat atg aaa gtt caa aca	1715
Phe Glu Gln His Cys Lys Met Ala Gln Glu Tyr Met Lys Val Gln Thr	
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gaa att gca ttg tta tta cag aga aag caa gaa cta gtt gca gaa ctg	1763

Glu Ile Ala Leu Leu Leu Gln Arg Lys Gln Glu Leu Val Ala Glu Leu
 515 520 525

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 Asp Gln Asp Glu Lys Asp Gln Gln Asn Thr Ser Arg Leu Val Gln Glu
 530 535 540

cat aaa aag ctt tta gat gaa aac aaa agc ctt tct act tac tac cag 1859
 His Lys Lys Leu Leu Asp Glu Asn Lys Ser Leu Ser Thr Tyr Tyr Gln
 545 550 555

caa tgc aaa aaa caa cta gag gtc atc aga agt cag cag cag aaa cga 1907
 Gln Cys Lys Lys Gln Leu Glu Val Ile Arg Ser Gln Gln Gln Lys Arg
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caa ggc act tca tgattctctg ggaccggttac attttgaaat atgcaaagaa 1959
 Gln Gly Thr Ser

agactttttt tttaaggaaa ggaaaacctt ataatgacga ttcattgagt ttagcttttt 2019

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Ile Glu Ser Glu Ser Glu Arg Lys Ala Phe Ile Val Glu Leu Arg Gln		
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Leu Ser Arg Val Asn His Pro Asn Ile Val Lys Leu Tyr Gly Ala Cys		
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Leu Asn Pro Val Cys Leu Val Met Glu Tyr Ala Glu Gly Gly Ser Leu		
	100	105 110
Tyr Asn Val Leu His Gly Ala Glu Pro Leu Pro Tyr Tyr Thr Ala Ala		
	115	120 125
His Ala Met Ser Trp Cys Leu Gln Cys Ser Gln Gly Val Ala Tyr Leu		
	130	135 140
His Ser Met Gln Pro Lys Ala Leu Ile His Arg Asp Leu Lys Pro Pro		
	145	150 155 160
Asn Leu Leu Leu Val Ala Gly Gly Thr Val Leu Lys Ile Cys Asp Phe		
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Gly Thr Ala Cys Asp Ile Gln Thr His Met Thr Asn Asn Lys Gly Ser		
	180	185 190
Ala Ala Trp Met Ala Pro Glu Val Phe Glu Gly Ser Asn Tyr Ser Glu		
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Lys Cys Asp Val Phe Ser Trp Gly Ile Ile Leu Trp Glu Val Ile Thr		
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Arg Arg Lys Pro Phe Asp Glu Ile Gly Gly Pro Ala Phe Arg Ile Met		
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Trp Ala Val His Asn Gly Thr Arg Pro Pro Leu Ile Lys Asn Leu Pro		
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Lys Pro Ile Glu Ser Leu Met Thr Arg Cys Trp Ser Lys Asp Pro Ser		
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Gln Arg Pro Ser Met Glu Glu Ile Val Lys Ile Met Thr His Leu Met		
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Arg Tyr Phe Pro Gly Ala Asp Glu Pro Leu Gln Tyr Pro Cys Gln Tyr		
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Ser Asp Glu Gly Gln Ser Asn Ser Ala Thr Ser Thr Gly Ser Phe Met		
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Asp Ile Ala Ser Thr Asn Thr Ser Asn Lys Ser Asp Thr Asn Met Glu		
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Gln Val Pro Ala Thr Asn Asp Thr Ile Lys Arg Leu Glu Ser Lys Leu		

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Gly Ala Ser His Gly Ser Ser Val Glu Ser Leu Pro Pro Thr Ser Glu		
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Gly Lys Arg Met Ser Ala Asp Met Ser Glu Ile Glu Ala Arg Ile Ala		
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Thr Val Thr Gly Thr Glu Pro Gly Gln Val Ser Ser Arg Ser Ser Ser		
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Pro Ser Val Arg Met Ile Thr Thr Ser Gly Pro Thr Ser Glu Lys Pro		
435	440	445
Thr Arg Ser His Pro Trp Thr Pro Asp Asp Ser Thr Asp Thr Asn Gly		
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465	470	475 480
Gln Pro Leu Ala Pro Cys Pro Asn Ser Lys Glu Ser Met Ala Val Phe		
485	490	495
Glu Gln His Cys Lys Met Ala Gln Glu Tyr Met Lys Val Gln Thr Glu		
500	505	510
Ile Ala Leu Leu Leu Gln Arg Lys Gln Glu Leu Val Ala Glu Leu Asp		
515	520	525
Gln Asp Glu Lys Asp Gln Gln Asn Thr Ser Arg Leu Val Gln Glu His		
530	535	540
Lys Lys Leu Leu Asp Glu Asn Lys Ser Leu Ser Thr Tyr Tyr Gln Gln		
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<220>
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cac ctc tct ggg gtt ggc tca gcc tcc aac cgc agc tac tct gct gat	149	
His Leu Ser Gly Val Gly Ser Ala Ser Asn Arg Ser Tyr Ser Ala Asp		
25 30 35 40		
ggc aag ggc act gag agc cac ccg cca gag gac agc tgg ctc aag ttc	197	
Gly Lys Gly Thr Glu Ser His Pro Pro Glu Asp Ser Trp Leu Lys Phe		
45 50 55		
agg agt gag aac aac tgc ttc ctg tat ggg gtc ttc aac ggc tat gat	245	
Arg Ser Glu Asn Asn Cys Phe Leu Tyr Gly Val Phe Asn Gly Tyr Asp		
60 65 70		
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Gly Asn Arg Val Thr Asn Phe Val Ala Gln Arg Leu Ser Ala Glu Leu		
75 80 85		
ctg ctg ggc cag ctg aat gcc gag cac gcc gag gcc gat gtg cgg cgt	341	
Leu Leu Gly Gln Leu Asn Ala Glu His Ala Glu Ala Asp Val Arg Arg		
90 95 100		
gtg ctg ctg cag gcc ttc gat gtg gtg gag agg agc ttc ctg gag tcc	389	
Val Leu Leu Gln Ala Phe Asp Val Val Glu Arg Ser Phe Leu Glu Ser		
105 110 115 120		
att gac gac gcc ttg gct gag aag gca agc ctc cag tcg caa ttg cca	437	
Ile Asp Asp Ala Leu Ala Glu Lys Ala Ser Leu Gln Ser Gln Leu Pro		
125 130 135		
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Glu Gly Val Pro Gln His Gln Leu Pro Pro Gln Tyr Gln Lys Ile Leu		
140 145 150		
gag aga ctc aag acg tta gag agg gaa att tcg gga ggg gcc atg gcc	533	
Glu Arg Leu Lys Thr Leu Glu Arg Glu Ile Ser Gly Gly Ala Met Ala		
155 160 165		
gtt gtg gcg gtc ctt ctc aac aac aag ctc tac gtc gcc aat gtc ggt	581	
Val Val Ala Val Leu Leu Asn Asn Lys Leu Tyr Val Ala Asn Val Gly		
170 175 180		
aca aac cgt gca ctt tta tgc aaa tcg aca gtg gat ggg ttg cag gtg	629	
Thr Asn Arg Ala Leu Leu Cys Lys Ser Thr Val Asp Gly Leu Gln Val		
185 190 195 200		
aca cag ctg aac gtg gac cac acc aca gag aac gag gat gag ctc ttc	677	
Thr Gln Leu Asn Val Asp His Thr Thr Glu Asn Glu Asp Glu Leu Phe		
205 210 215		

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aaa tat ggc tac acg gac att gac ctt ctc agc gct gcc aag tcc aaa Lys Tyr Gly Tyr Thr Asp Ile Asp Leu Leu Ser Ala Ala Lys Ser Lys 250 255 260	821
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gtg acg ggc ttc ttg gtg ctg atg tcg gag ggg ttg tac aag gcc cta Val Thr Gly Phe Leu Val Leu Met Ser Glu Gly Leu Tyr Lys Ala Leu 285 290 295	917
gag gca gcc cat ggg cct ggg cag gcc aac cag gag att gct gcg atg Glu Ala Ala His Gly Pro Gly Gln Ala Asn Gln Glu Ile Ala Ala Met 300 305 310	965
att gac act gag ttt gcc aag cag acc tcc ctg gac gca gtg gcc cag Ile Asp Thr Glu Phe Ala Lys Gln Thr Ser Leu Asp Ala Val Ala Gln 315 320 325	1013
gcc gtc gtg gac cgg gtg aag cgc atc cac agc gac acc ttc gcc agt Ala Val Val Asp Arg Val Lys Arg Ile His Ser Asp Thr Phe Ala Ser 330 335 340	1061
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cta gtg agg aac ttt ggc tac ccg ctg ggc gaa atg agc cag ccc aca Leu Val Arg Asn Phe Gly Tyr Pro Leu Gly Glu Met Ser Gln Pro Thr 365 370 375	1157
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cca tac tcc agc gcc cag agc acc agc aag acc agc gtg acc ctc tcc Pro Tyr Ser Ser Ala Gln Ser Thr Ser Lys Thr Ser Val Thr Leu Ser 395 400 405	1253
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tcc acc ctg gac gaa gcc acc ccc acc ctc acc aac caa agc ccg acc Ser Thr Leu Asp Glu Ala Thr Pro Thr Leu Thr Asn Gln Ser Pro Thr 425 430 435 440	1349
tta acc ctg cag tcc acc aac acg cac acg cag agc agc agc tcc agc	1397

Leu Thr Leu Gln Ser Thr Asn Thr His Thr Gln Ser Ser Ser Ser Ser
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 Ser Asp Gly Gly Leu Phe Arg Ser Arg Pro Ala His Ser Leu Pro Pro
 460 465 470
 ggc gag gac ggt cgt gtt gag ccc tat gtg gac ttt gct gag ttt tac 1493
 Gly Glu Asp Gly Arg Val Glu Pro Tyr Val Asp Phe Ala Glu Phe Tyr
 475 480 485
 cgc ctc tgg agc gtg gac cat ggc gag cag agc gtg gtg aca gca ccg 1541
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 <213> Homo sapiens

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 35 40 45
 Pro Glu Asp Ser Trp Leu Lys Phe Arg Ser Glu Asn Asn Cys Phe Leu
 50 55 60
 Tyr Gly Val Phe Asn Gly Tyr Asp Gly Asn Arg Val Thr Asn Phe Val
 65 70 75 80
 Ala Gln Arg Leu Ser Ala Glu Leu Leu Leu Gly Gln Leu Asn Ala Glu
 85 90 95
 His Ala Glu Ala Asp Val Arg Arg Val Leu Leu Gln Ala Phe Asp Val
 100 105 110
 Val Glu Arg Ser Phe Leu Glu Ser Ile Asp Asp Ala Leu Ala Glu Lys
 115 120 125
 Ala Ser Leu Gln Ser Gln Leu Pro Glu Gly Val Pro Gln His Gln Leu
 130 135 140
 Pro Pro Gln Tyr Gln Lys Ile Leu Glu Arg Leu Lys Thr Leu Glu Arg
 145 150 155 160
 Glu Ile Ser Gly Gly Ala Met Ala Val Val Ala Val Leu Leu Asn Asn
 165 170 175

Lys Leu Tyr Val Ala Asn Val Gly Thr Asn Arg Ala Leu Leu Cys Lys
 180 185 190
 Ser Thr Val Asp Gly Leu Gln Val Thr Gln Leu Asn Val Asp His Thr
 195 200 205
 Thr Glu Asn Glu Asp Glu Leu Phe Arg Leu Ser Gln Leu Gly Leu Asp
 210 215 220
 Ala Gly Lys Ile Lys Gln Val Gly Ile Ile Cys Gly Gln Glu Ser Thr
 225 230 235 240
 Arg Arg Ile Gly Asp Tyr Lys Val Lys Tyr Gly Tyr Thr Asp Ile Asp
 245 250 255
 Leu Leu Ser Ala Ala Lys Ser Lys Pro Ile Ile Ala Glu Pro Glu Ile
 260 265 270
 His Gly Ala Gln Pro Leu Asp Gly Val Thr Gly Phe Leu Val Leu Met
 275 280 285
 Ser Glu Gly Leu Tyr Lys Ala Leu Glu Ala Ala His Gly Pro Gly Gln
 290 295 300
 Ala Asn Gln Glu Ile Ala Ala Met Ile Asp Thr Glu Phe Ala Lys Gln
 305 310 315 320
 Thr Ser Leu Asp Ala Val Ala Gln Ala Val Val Asp Arg Val Lys Arg
 325 330 335
 Ile His Ser Asp Thr Phe Ala Ser Gly Gly Glu Arg Ala Arg Phe Cys
 340 345 350
 Pro Arg His Glu Asp Met Thr Leu Leu Val Arg Asn Phe Gly Tyr Pro
 355 360 365
 Leu Gly Glu Met Ser Gln Pro Thr Pro Ser Pro Ala Pro Ala Ala Gly
 370 375 380
 Gly Arg Val Tyr Pro Val Ser Val Pro Tyr Ser Ser Ala Gln Ser Thr
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 Ser Lys Thr Ser Val Thr Leu Ser Leu Val Met Pro Ser Gln Gly Gln
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 Met Val Asn Gly Ala His Ser Ala Ser Thr Leu Asp Glu Ala Thr Pro
 420 425 430
 Thr Leu Thr Asn Gln Ser Pro Thr Leu Thr Leu Gln Ser Thr Asn Thr
 435 440 445
 His Thr Gln Ser Ser Ser Ser Ser Ser Asp Gly Gly Leu Phe Arg Ser
 450 455 460
 Arg Pro Ala His Ser Leu Pro Pro Gly Glu Asp Gly Arg Val Glu Pro
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 485 490 495

Glu Gln Ser Val Val Thr Ala Pro
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 <212> DNA
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 <212> DNA
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<210> 7
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 <212> DNA
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